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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 04:25:46 ; Search time 93 Seconds
(without alignments)
420.956 Million cell updates/sec

Title: US-09-895-298A-83
Perfect score: 1002
Sequence: 1 MMNFQPPSKAWRASQMMTF.....HDGSLDLRSRSVQEGNRA 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriophage:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1002	100.0	330	4 Q9H8I7	Q9h8i7 homo sapien
2	857	85.5	757	11 Q9D4F1	Q9d4f1 mus musculu
3	292.5	29.2	444	4 Q43284	Q43284 homo sapien
4	292.5	29.2	811	4 Q8TE07	Q8teq7 homo sapien
5	287.5	28.7	450	11 Q99J32	Q99j32 mus musculu
6	186.5	18.6	373	11 Q99K19	Q99k19 mus musculu
7	118	11.8	402	4 Q9H766	Q9h766 homo sapien
8	107.5	10.7	1247	5 Q966F8	Q966f8 caenorhabdi
9	99.5	9.9	888	11 Q8R4P4	Q8r4p4 mus musculu
10	97.5	9.7	282	11 Q8R1X9	Q8r1x9 mus musculu
11	97	9.7	214	4 Q9BYN5	Q9byn5 homo sapien
12	97	9.7	890	4 Q8TD17	Q8td17 homo sapien
13	94.5	9.4	451	16 Q97MN0	Q97mn0 clostridium
14	91.5	9.1	279	11 Q9D435	Q9d435 mus musculu
15	91.5	9.1	757	11 Q8R4P5	Q8r4p5 mus musculu
16	90.5	9.0	760	4 Q8TD18	Q8td18 homo sapien

17	88.5	8.8	706	4 Q8TBS7	Q8tbs7 homo sapien
18	88	8.8	322	16 Q07420	Q07420 mycobacteri
19	87.5	8.7	261	5 Q18875	Q18875 caenorhabdi
20	87	8.7	272	10 Q9M0B7	Q9m0b7 arabidopsis
21	86.5	8.6	365	17 Q8TM73	Q8tm73 methanosarc
22	84.5	8.4	713	16 Q9KG35	Q9kg35 bacillus ha
23	84	8.4	148	10 Q8S8N8	Q8s8n8 arabidopsis
24	84	8.4	273	10 Q8S8O6	Q8s8o6 arabidopsis
25	81.5	8.1	154	16 Q92AG4	Q92ag4 listeria in
26	81.5	8.1	204	16 Q8YOG8	Q8yog8 anabaena sp
27	81	8.1	264	9 Q8SBD6	Q8sbd6 staphylococ
28	80.5	8.0	200	16 Q9KCU0	Q9kcu0 bacillus ha
29	80.5	8.0	267	17 Q9HJU3	Q9hju3 thermoplasm
30	80	8.0	203	16 Q99ZE3	Q99ze3 streptococc
31	80	8.0	378	3 Q12006	Q12006 saccharomyc
32	80	8.0	443	8 Q33559	Q33559 leishmania
33	79.5	7.9	154	16 Q8Y656	Q8y656 listeria mo
34	79.5	7.9	217	16 Q8ZSC1	Q8zsc1 anabaena sp
35	79.5	7.9	396	16 Q99V76	Q99v76 staphylococ
36	79.5	7.9	476	5 Q8T1Y3	Q8t1y3 dictyosteli
37	79.5	7.9	589	16 Q9L2K4	Q9l2k4 streptomyce
38	79.5	7.9	704	5 Q8T1P6	Q8t1p6 dictyosteli
39	79.5	7.9	772	16 Q97LD1	Q97ld1 clostridium
40	79.5	7.9	913	5 Q97272	Q97272 plasmodium
41	79	7.9	218	5 Q9N895	Q9n895 plasmodium
42	79	7.9	239	16 Q8Z8B7	Q8z8b7 salmonella
43	78.5	7.8	329	16 Q99RY0	Q99ry0 staphylococ
44	78	7.8	319	5 Q9XV63	Q9xv63 caenorhabdi
45	78	7.8	552	5 Q95QK9	Q95qk9 caenorhabdi

ALIGNMENTS

RESULT 1

Q9H8I7 PRELIMINARY; PRT; 330 AA.
ID Q9H8I7;
AC Q9H8I7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CDNA FLJ13593 fis, clone PLACE109493.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiraori A., Sudo H., Sugawara M.,
RA Wagatsuma M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Takiguchi S.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Saito K.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Masuo Y.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuo Y.,
RA Ninomiya K., Iwayanagi T.,
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK023655; BAB14629.1; -
SQ SEQUENCE 330 AA; 38958 MW; EBA21A1AC1A55C2E CRC64;

Query Match 100.0%; Score 1002; DB 4; Length 330;
Best local similarity 100.0%; Pred. No. 3.8e-87;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMNFQPPSKAWRASQMMTFEFLPEPSFTGVCTIATITWRLKPSADCGPFGLEPIH 60
DB 141 MMNFQPPSKAWRASQMMTFEFLPEPSFTGVCTIATITWRLKPSADCGPFGLEPIH 200
QY 61 SIYSWITLSTRPGYLWVWVYIRNLIGSVHFFILFLIVLITLYLWQTEGRKIMIRLL 120
DB 201 SIYSWITLSTRPGYLWVWVYIRNLIGSVHFFILFLIVLITLYLWQTEGRKIMIRLL 260


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QY      1 MANNOPPSKAMRASOMMTFFILFLFPDPSFTGVLCTLAITWRLKPSADCGPFRGLPLFIH 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      639 LANCQAPRRPWLASHMSTVFLLTLCCEPAFLGAAVFLCYAAMQVKPSSTCGPFRLDTMYE 698

QY      61 SIYSWIDTL-STRGYLWVWVIYRNIGSVHFFILTLIYLITLYWQITEGKRIMIRL 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      699 AGRVWVRHLAEAGPRVSVLPWVHRVYLMENTFEYFLVSALLAVIYLNIGQVVRGORKVICL 758

QY      120 LHEOIINEGDKMFLIEKLKLOD-----MEKANPSSVILERR 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      759 LKEQIISNEGEDIKFLINKKHSIYERKERERERSRVGTTEEAAPALLTDEOD 810

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RESULT 5		
O99J32		
ID	O99J32	PRELIMINARY; PRT; 450 AA.
AC	O99J32;	
DT	01-JUN-2001 (TREMBLrel. 17, Created)	
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	Similar to expressed in activated T/LAK lymphocytes (Hypothetical 51.0 kDa protein).	
DE	Mus musculus (Mouse).	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	

RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases
DR EMBL; BC004840; AAH04840.1; -.
DR EMBL; BC013502; AAH13502.1; -.
DR InterPro; IPR000515; BPD_transp.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBR; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 450 AA; 51009 MW; AF19129C11A53BD0 CRC64;

[illegible]

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Qy 120 LHEQIINEGKDKMFLIEKLKIQDEKKANP 150
    | | | | | : | : |
Db 392 LKEQIRNEGDKIFLINKLHVSVEEGRSRP 422
```

RESULT	6
O99K19	
ID	O99K19
AC	O99K19; PRELIMINARY; PRT; 373 AA.
DT	01-JUN-2001 (TRMBLrel. 17, Created)
DT	01-JUN-2001 (TRMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TRMBLrel. 19, Last annotation update)
DE	Hypothetical 42.3 kDa protein (Unknown) (Protein for MGC:12049).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.

RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases
DR EMBL; BC005510; AAH05510.1; -
DR EMBL; BC006956; AAH06956.1; -
DR InterPro; IPR000515; BPD_transp.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 373 AA; 42254 MW; 13B4C5E8A0FFB889 CRC64;

	Query Match	18.6%;	Score 186.5;	DB 11;	Length 373;
	Best Local Similarity	35.6%;	Pred. No. 1.le-09;		
	Matches 36; Conservative	18;	Mismatches 46;	Indels 1;	Gaps 1:
QY	1	MMNQPPSKAMRASQMTEFFLLFEFSGVCLTLATITWRKPSADCCGPRGLPLEIH	60		
	:	:	:	: : :	
Dd	272	MANCQAPRRPWLASHMSTVFLLTLCFPFLGAAVELCYAWQVRPSSTCGPRTLNTMYE	331		
QY	61	SIVSMDLTLS-TRPGYLWVVVIYRNLIGSVHFEFFILTIVL	100		
	:	:	:	:	:
Dd	332	AGTVAVVRRLRHAGSGASWLPWIHLHVIENTFFFLASALLL	372		

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RESULT 7
Q9H766
ID Q9H766 PRELIMINARY; PRT; 402 AA.
AC Q9H766;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CDNA: FLJ21240 fis, clone COL01132.
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shidahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
SQ EMBL: AK024893; BAB15032.1; - 716C11B5B794DC4 CRC64;
SQ SEQUENCE 402 AA; 46254 MW; 716C11B5B794DC4 CRC64;

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Query Match	11.88;	Score 118;	DB 4;	Length 402;
Best Local Similarity	26.33;	Pred. No. 0.0036;		
Matches 40;	Conservative 29;	Mismatches 53;	Indels 30;	Gaps
QY	5	QPPSKAMRASQMMTFEIFFLLFPSTGVCLTATITWLKESADCGPF-----R	53	
DB	267	RSPRRPRRASNSNFFLLVLLIGLCIAII-PLTISISIRIPSSKACGPFNTNFTWEVIRP	325	
QY	54	GLPLFIHSIYWDITLSTRPGYLVWVIVYRNLIQSVHFFFTLLIVLITTYLWOITEGR	113	
DB	326	TVSTFPSLSQSFTHGVTSF-----AFVVPFMTICLIM---FYIALAGAH	368	
QY	114	KIMIRLLHEQIINEGKDKMFLIEKLIRQ-DM	144	
DB	369	KRVVIOQLREQLSLESRDCKYLIQKLTAEQRDM	400	

RESULT 8	
Q966F8	
ID	Q966F8
AC	Q966F8;
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Hypothetical protein T13G4.3.
GN T13G4.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
OC Rhabdilitidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Favello T.;
RT "The sequence of C. elegans cosmid T13G4.";
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC006685; AAK84572.1;
SQ SEQUENCE 1247 AA; 142928 MW; F0BB43BA38721E49 CRC64;

Query Match 10.7%; Score 107.5; DB 5; Length 1247;
Best Local Similarity 26.5%; Pred. No. 0.11;
Matches 49; Conservative 32; Mismatches 75; Indels 29; Gaps 8;

QY 6 PPSKAMRASQMTFFIFLFPSPFTGVLCTLAITWRLKPSADCGPFRGLPLFIHSIY 63
DB 736 PAREIFRASRSSNFFYLGLIL--IWLLCTLPVGVIASMSPSRSCGP-----ARY 784
QY 64 SWIDTLSTRPGYLWV--WVYRNIGSVHFFILTLVLIITYLWQITEGRK-----I 115
DB 785 QHFTVYVTRIEIKRVDQVLYSIYRHTASPGVPIPIILLIITYFLFSVLVGLREANTDL 844
QY 116 MIRLHEQIINEGDKMFLI-----EKLIKDMEKKANPSSLVERREVEQGFHLHGE 170
DB 845 QAQLVHER--TEKKKIFELAGGKKNKEKDRD-KKRSNDYIPLIEORRRRPPWRQYHEME 901
QY 171 HDGSL 175
DB 902 ADHAL 906

RESULT 9
Q8R4P4 PRELIMINARY; PRT; 888 AA.
AC Q8R4P4;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Transmembrane cochlear-expressed protein 2.
GN TMC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918583; PubMed=11850618;
RA Kurima K., Peters L.M., Yang Y., Riazuddin S., Ahmed Z.M., Naz S.,
Arnaud D., Drury S., Mo J., Makishima T., Ghosh M., Menon P.S.N.,
Radeshmukh D., Oddoux C., Ostrer H., Khan S., Riazuddin S.,
Dehlinger P.L., Hampton L.L., Sullivan S.L., Batley J.F.,
Keats B.J.B., Wilcox E.R., Friedman T.B., Griffith A.U.;
RT "Dominant and recessive deafness caused by mutations of a novel gene,
TMC1, regulated for cochlear hair-cell function.";

RL Nat. Genet. 30:277-284(2002).
DR EMBL; AF417581; AAL86402.1;
SQ SEQUENCE 888 AA; 101134 MW; 6D834D7987768FA7 CRC64;

Query Match 9.9%; Score 99.5; DB 11; Length 888;
Best Local Similarity 21.5%; Pred. No. 0.46;
Matches 51; Conservative 33; Mismatches 72; Indels 81; Gaps 10;

QY 6 PPSKAMRASQMTFFIFLFPSPFTGVLCTLAITWRLKPSADCGPFRG-----54
DB 663 PHERVERASRSNNFFYMGILLVLFSL--PVAITYMSLPPSFCGPFSGKNRMVDYIHE 721
QY 55 ----LPLFIHSIYSWIDTLSTRPGYLWVWYRNIGSVHFFILTLVLIITYLWQIT 110
DB 722 IENDPFRFLGKIFAF--ANP-----LIIPAILMFLAIFYLNS 759
QY 111 EGRKI-----MIRLHEQIIN--EGDKMFLIEKLK-----140
DB 760 VSKSLSRANAQLRKRKIQALREVEKNHKSIGKRAIVTYS EDTIKNSSKNAQIHLTRKEPT 819
QY 141 -----LQDMEKRA-NPSSLVERREVEQGFHLGHDGSLDRSRVQEGNPRA 190
DB 820 SHSSSQIOTLDKRAQGPHTSTEGGASPTSMHHV-----GSGPFRGR--DSGQPOS 870

RESULT 10
Q8R1X9 PRELIMINARY; PRT; 282 AA.
AC Q8R1X9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 31.3 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SALIVARY GLAND;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC022758; AAH22758.1;
FT NON_TER 1
SQ SEQUENCE 282 AA; 31318 MW; 0E062E6ED7645C7C CRC64;

Query Match 9.7%; Score 97.5; DB 11; Length 282;
Best Local Similarity 28.3%; Pred. No. 0.22;
Matches 43; Conservative 25; Mismatches 49; Indels 35; Gaps 7;

QY 4 FQPPSKAMRASQMTFFIFLFPSPFTGVLCTLAITWRLKPSADCGPFRGLP 56
DB 145 YSPASRTFRASTANFFPLV-----LVGLAISAVPVLYSIFLIPPSKLCGPFPGKL 196
QY 57 LFIHSIYSWIDTLSTRPGYLWVWYRNIGSVHFFILTLVLIITYLWQIT-----110
DB 197 SIWAQLEPAIESLPQTAQNFLY-----FLGTQAF-----TVPILLISILMYTVALAN 245
QY 111 -EGRKIMIRLHEQIINEGDKMFLIEKLK 141
DB 246 CYGR--LISELKRQIETEVQNKVFLAQRAVAL 275

RESULT 11
Q9BYN5 PRELIMINARY; PRT; 214 AA.
AC Q9BYN5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Df686c3.6 (Novel protein) (Fragment).
GN Df686c3.3.

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL Smith M.;
DR Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AL049712; CAC29096.1; -.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 214 AA; 24357 MW; 079641A43CC112A7 CRC64;

Query Match
Best Local Similarity 9.7%; Score 97; DB 4; Length 214;
Matches 29; Conservative 18; Mismatches 32; Indels 38; Gaps 4;

QY 6 PPSKAWRASQMTFFILLFPSPFTGVCTLATIIRLKPADCGPFRG----- 54
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 100 PHERYFKASNSNNFYMGILLVLFLSL-LPVAYTMSLPSPFDCGPGSKNMYDVIQET 158
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 55 ----LPLFHSIYSWIDTLPSTPGYLWVWYIRNLIGSVHFFILLIVLITTYLW 107
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 159 IENDEPTFLCKIFAFL---ANPG-----LIIPIALLMFLAIYY 193
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 12
Q8TDT7
ID Q8TDT7 PRELIMINARY; PRT; 890 AA.
AC Q8TDT7;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Transmembrane cochlear-expressed protein 2.
GN TMC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918583; PubMed=11850618;
RA Kurita K., Peters L.M., Yang Y., Riazuddin S., Ahmed Z.M., Naz S.,
RA Arnaud D., Drury S., Mo J., Makishima T., Ghosh M., Menon P.S.N.,
RA Deshmukh D., Oddoux C., Ostler H., Khan S., Riazuddin S.,
RA Dehlinger P.L., Hampton L.L., Sullivan S.L., Battey J.F.,
RA Keats B.J.B., Wilcox E.R., Friedman T.B., Griffith A.J.;
RT "Dominant and recessive deafness caused by mutations of a novel gene,
RT TMC1, required for cochlear hair-cell function.";
RL Nat. Genet. 30:277-284(2002).
DR EMBL; AF417580; AAL86401.1; -.
SQ SEQUENCE 890 AA; 101006 MW; A35AE2216B2AC0C4 CRC64;

Query Match
Best Local Similarity 9.7%; Score 97; DB 4; Length 890;
Matches 29; Conservative 18; Mismatches 32; Indels 38; Gaps 4;

QY 6 PPSKAWRASQMTFFILLFPSPFTGVCTLATIIRLKPADCGPFRG----- 54
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 665 PHERYFKASNSNNFYMGILLVLFLSL-LPVAYTMSLPSPFDCGPGSKNMYDVIQET 723
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 55 ----LPLFHSIYSWIDTLPSTPGYLWVWYIRNLIGSVHFFILLIVLITTYLW 107
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 724 IENDEPTFLCKIFAFL---ANPG-----LIIPIALLMFLAIYY 758
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 13
Q97MNO
ID Q97MNO PRELIMINARY; PRT; 451 AA.
AC Q97MNO;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)

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[illegible]

